

SEQUENCE LISTING

<110> Alan Brash
Nathalie Tijet

<120> MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE
LYASE AND USES THEREOF

<130> 06027.0002

<160> 56

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 10
<212> PRT
<213> Cucumis melo

<400> 1
Met Ala Thr Pro Ser Ser Ser Ser Pro Glu
1 5 10

<210> 2
<211> 15
<212> PRT
<213> Cucumis melo

<400> 2
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1 5 10 15

<210> 3
<211> 8
<212> PRT
<213> Cucumis melo

<400> 3
Arg Leu Phe Leu Ser Phe Leu Ala
1 5

<210> 4
<211> 7
<212> PRT
<213> Cucumis melo

<400> 4
Ser Ile Ser Asp Ser Met Ser
1 5

<210> 5
<211> 8
<212> PRT

Lys Val Leu Phe Pro Thr Leu Leu Lys Trp Val Gly Thr Ala Gly Glu
 290 295 300
 Asp Leu His Arg Lys Leu Ala Glu Glu Val Arg Thr Thr Val Lys Glu
 305 310 315 320
 Glu Gly Gly Leu Thr Phe Ser Ala Leu Glu Lys Met Ser Leu Leu Lys
 325 330 335
 Ser Val Val Tyr Glu Ala Leu Arg Ile Glu Pro Pro Val Pro Phe Gln
 340 345 350
 Tyr Gly Lys Ala Lys Glu Asp Ile Val Ile Gln Ser His Asp Ser Ser
 355 360 365
 Phe Lys Ile Lys Lys Gly Glu Thr Ile Phe Gly Tyr Gln Pro Phe Ala
 370 375 380
 Thr Lys Asp Pro Lys Ile Phe Lys Asp Ser Glu Lys Phe Val Gly Asp
 385 390 395 400
 Arg Phe Val Gly Glu Glu Gly Glu Lys Leu Lys Tyr Val Tyr Trp
 405 410 415
 Ser Asn Glu Arg Glu Thr Val Glu Pro Thr Ala Glu Asn Lys Gln Cys
 420 425 430
 Pro Gly Lys Asn Leu Val Val Leu Ile Gly Arg Ile Met Val Val Glu
 435 440 445
 Phe Phe Leu Arg Tyr Asp Thr Phe Thr Val Glu Val Ala Asp Leu Pro
 450 455 460
 Leu Gly Pro Ala Val Lys Phe Lys Ser Leu Thr Arg Ala Thr Asp Met
 465 470 475 480
 Val

<210> 8

<211> 1446

<212> DNA

<213> Cucumis melo

<400> 8

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gacgaattct	tccgttcccc	gattacaaaa	tacaactcca	ccgtcttccg	cgccaacatg	180
ccaccggggc	ccttcatttc	ctccgattcc	agagtcgttg	tccttctcga	tgccttcagt	240
tttctatcc	tcttcgacac	agccaaagtc	gagaaaacga	acattctcga	cggaacttac	300
atgccctcct	tgtccttcac	cggcaacatt	cgcacctgtg	cttatttgga	cccatcggaa	360
acagagcact	ctgttctcaa	acgcctcttc	ctctcctttc	tcgcttcccg	ccatgacagg	420
ttcatccctc	tgtttcgaag	ctccttgtct	gagatgtttg	ttaagcttga	agataaaactt	480
tccgagaaaa	agaagatcgc	tgatttcaac	tcgatcagcg	attccatgtc	gtttgattat	540
gttttcctgt	tactctccga	tggaaacccct	gattcgaaat	tagctgctga	gggacctgga	600
atgttcgatc	tgtggcttgt	gtttcaactc	gccccattgg	cttccattgg	ccttcccaaa	660
attttctctg	tttttgaaga	tctcgtcatt	cacaccattc	ccctgccttt	cttcccagtc	720
aagagtgggt	acaggaagct	ttatgaagcg	ttttactcct	cttctggctc	atttctagac	780
gaagcagaga	aacaggggat	agacagggag	aaagcatgtc	acaatttagt	gtttctcgct	840
ggattcaacg	catacggggg	aatgaaagtc	ctttttccca	ctttactgaa	atgggctcggc	900
accgccggcg	aggatctcca	cgggaaactc	gccgaggaag	tcaggacaac	cgtgaaggaa	960
gaagggggac	tgactttctc	cgccttggag	aaaatgagtc	tgctgaagtc	cgtcgtgtac	1020
gaagcactca	ggatcgaacc	gccgggtgcc	ttccagtacg	ggaaagcgaa	ggaggatatc	1080
gtgattcaga	gccacgattc	ttctttcaag	atcaaaaaag	gggagacgat	ttttggttat	1140
cagccgtttg	ctactaaaga	tccgaagatt	tttaaggatt	cggagaagtt	cgtgggcgat	1200
aggttcgtgg	gagaggaagg	ggagaagctt	ttgaagtatg	tttactggtc	aaatgagcgg	1260
gagacagtgg	agccgacggc	ggagaacaag	cagtgtccgg	ggaagaatct	gggtggtgctg	1320
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<210> 9
<211> 60
<212> PRT
<213> Psidium Guava
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<210> 10
<211> 61
<212> PRT
<213> Banana
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```
<210> 11
<211> 62
<212> PRT
<213> Capsicum annum (green pepper)
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<210> 12
<211> 62
<212> PRT
<213> Arabidopsis
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<400> 12
Gly Glu Met Leu Tyr Gly Tyr Gln Pro Leu Ala Thr Arg Asp Pro Lys
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```

```
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<211> 61
<212> PRT
<213> Flax
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<210> 14
<211> 61
<212> PRT
<213> Guayule
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<210> 15
<211> 487
<212> PRT
<213> Cucumis melo
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<221> VARIANT
<222> (1)...(487)
<223> Xaa = Any Amino Acid

<221> misc_feature
<222> (0)...(0)
<223> Accession No. AF081955
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<400> 15
Met Ala Thr Pro Ser Ser Ser Ser Pro Glu Leu Pro Leu Lys Pro Ile
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Pro Gly Gly Tyr Gly Phe Pro Phe Leu Gly Pro Ile Lys Asp Arg Tyr
      20              25              30

```

Asp	Tyr	Phe	Tyr	Phe	Gln	Gly	Arg	Asp	Glu	Phe	Phe	Glu	Arg	Ser	Arg
		35					40				45				
Ile	Thr	Lys	Tyr	Asn	Ser	Thr	Val	Phe	Arg	Ala	Asn	Met	Pro	Pro	Gly
	50					55					60				
Pro	Phe	Ile	Ser	Ser	Asp	Ser	Arg	Val	Val	Val	Leu	Leu	Asp	Ala	Leu
65					70					75					80
Ser	Phe	Pro	Ile	Leu	Phe	Asp	Thr	Ala	Lys	Val	Glu	Lys	Arg	Asn	Ile
				85					90					95	
Leu	Asp	Gly	Thr	Tyr	Met	Pro	Ser	Leu	Ser	Phe	Thr	Gly	Asn	Ile	Arg
			100					105					110		
Thr	Cys	Ala	Tyr	Leu	Asp	Pro	Ser	Glu	Thr	Glu	His	Ser	Val	Leu	Lys
		115					120					125			
Arg	Leu	Phe	Leu	Ser	Phe	Leu	Ala	Ser	Arg	His	Asp	Arg	Phe	Ile	Pro
	130					135					140				
Leu	Phe	Arg	Ser	Ser	Leu	Ser	Glu	Met	Phe	Val	Lys	Leu	Glu	Asp	Lys
145					150					155					160
Leu	Ser	Glu	Lys	Lys	Lys	Ile	Ala	Asp	Phe	Asn	Ser	Ile	Ser	Asp	Ser
				165					170					175	
Met	Ser	Phe	Asp	Tyr	Val	Phe	Arg	Leu	Leu	Ser	Asp	Gly	Thr	Pro	Asp
			180					185					190		
Ser	Lys	Leu	Ala	Ala	Glu	Gly	Pro	Gly	Met	Phe	Asp	Leu	Trp	Leu	Val
		195					200					205			
Phe	Gln	Leu	Ala	Pro	Leu	Ala	Ser	Ile	Gly	Leu	Pro	Lys	Ile	Phe	Ser
	210					215					220				
Val	Phe	Glu	Asp	Leu	Val	Ile	His	Thr	Ile	Pro	Leu	Pro	Phe	Phe	Pro
225					230					235					240
Val	Lys	Ser	Gly	Tyr	Arg	Lys	Leu	Tyr	Glu	Ala	Phe	Tyr	Ser	Ser	Ser
				245						250				255	
Gly	Ser	Phe	Leu	Asp	Glu	Ala	Glu	Lys	Gln	Gly	Ile	Asp	Arg	Glu	Lys
			260					265					270		
Ala	Cys	His	Asn	Leu	Val	Phe	Leu	Ala	Gly	Phe	Asn	Ala	Tyr	Gly	Gly
		275					280					285			
Met	Lys	Val	Leu	Phe	Pro	Thr	Leu	Leu	Lys	Trp	Val	Gly	Thr	Ala	Gly
	290					295					300				
Glu	Asp	Leu	His	Arg	Lys	Leu	Ala	Glu	Glu	Val	Arg	Thr	Thr	Val	Lys
305					310					315					320
Glu	Glu	Gly	Gly	Leu	Thr	Phe	Ser	Ala	Leu	Glu	Lys	Met	Ser	Leu	Leu
				325					330					335	
Lys	Ser	Val	Val	Tyr	Glu	Ala	Leu	Arg	Ile	Glu	Pro	Pro	Val	Pro	Phe
			340					345					350		
Gln	Tyr	Gly	Lys	Ala	Lys	Glu	Asp	Ile	Val	Ile	Gln	Ser	His	Asp	Ser
		355					360					365			
Ser	Phe	Lys	Ile	Lys	Lys	Gly	Glu	Thr	Ile	Phe	Gly	Tyr	Gln	Pro	Phe
	370					375					380				
Ala	Thr	Lys	Asp	Pro	Lys	I									

Met Leu Lys Leu Met Thr Asn
485

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1) ... (23)
<223> n = A,T,C or G
y = C or T(U)

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 16
ggtgagttgc tntgyggnta yca

23

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1) ... (20)
<223> n = A,T,C or G
y = A,T,C or G

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 17
ggtgagttgc tntgyggnta

20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1) ... (20)
<223> n = A,T,C or G
y = C or T(U)

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 18
tggtcnaayg gncrcgagac

20

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<220>
<221> misc_feature
<222> (1)...(23)
<223> n = A,T,C or G
      y = C or T(U)
      r = A or G
```

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 19
tactgggtcna ayggncnrsa rac

23

```
<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence
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```
<220>
<221> misc_feature
<222> (1) ... (24)
<223> n = A, T, C or G
      y = C or T(U)
      r = A or G
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<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 20
aayaarcart gygçngctaa ggac

24

```
<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> misc_feature
<222> (1)...(21)
<223> n = A,T,C or G
      y = C or T(U)
      r = A or G
```

<223> Description of Artificial Sequence:/Note =
synthetic construct

```
<400> 21
aarcartgyg cngctaagga c
```

21

Variable	Mean	SD	Min	Max	Median	Mode	Skewness	Kurtosis	Shapiro-Wilk	Normality
Age	35.2	12.5	18	65	32	30	0.15	2.8	0.98	Normal
Gender	1.2	0.4	1	2	1	1	0.05	0.5	0.99	Normal
Marital Status	1.5	0.5	1	3	1	1	0.10	1.2	0.97	Normal
Education	12.5	2.5	9	16	12	12	0.05	0.8	0.99	Normal
Income	1500	500	500	3000	1200	1000	0.20	3.5	0.95	Normal
Occupation	1.8	0.6	1	3	1	1	0.05	0.5	0.99	Normal
Health Status	1.2	0.4	1	2	1	1	0.05	0.5	0.99	Normal
Stress Level	2.5	1.0	1	4	2	2	0.10	1.2	0.97	Normal
Life Satisfaction	3.5	1.5	1	5	3	3	0.05	0.8	0.99	Normal
Resilience	2.8	1.2	1	4	2	2	0.10	1.2	0.97	Normal
Emotional Stability	3.2	1.0	1	4	3	3	0.05	0.8	0.99	Normal
Physical Health	3.8	1.2	1	5	3	3	0.05	0.8	0.99	Normal
Mental Health	3.5	1.0	1	5	3	3	0.05	0.8	0.99	Normal
Overall Well-being	3.0	1.2	1	5	3	3	0.05	0.8	0.99	Normal

<210> 22
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 22
Gly Glu Leu Leu Cys Gly Tyr Gln
1 5

<210> 23
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 23
Gly Glu Leu Leu Cys Gly Tyr
1 5

<210> 24
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 24
Trp Ser Asn Gly Pro Glu Thr
1 5

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 25
Tyr Trp Ser Asn Gly Pro Glu Thr
1 5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

06027.0002

```
<210> 30
<211> 32
<212> PRT
<213> Cucumis melo
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[illegible]

<400> 30

Gly	Glu	Leu	Leu	Cys	Gly	Tyr	Gln	Pro	Phe	Ala	Thr	Lys	Asp	Pro	Lys
1				5					10				15		
Ile	Phe	Lys	Asp	Ser	Glu	Lys	Phe	Val	Gly	Asp	Arg	Phe	Val	Gly	Glu
			20					25					30		

<210> 31

<211> 272

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 31

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gtggcggact	gcgcacacat	gattgagtac	ttggggttat	taaagtaatt	tcgttgtgat	120
ccacgtggtc	ttattttaat	ttgagatctc	attgtgtgtt	gtaaccacc	ggtcattctta	180
ttttatagtt	tgtttgtttt	ctcaattatg	ctccaaattt	taaaataaat	aaataccatc	240
ttcttctttt	tactaaaaaa	aaaaaaaaaa	aa			272

<210> 32

<211> 480

<212> PRT

<213> Capsicum annum (green pepper)

<400> 32

Met	Ile	Pro	Ile	Met	Ser	Ser	Ala	Pro	Leu	Ser	Thr	Ala	Thr	Pro	Ile
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Ser	Leu	Pro	Val	Arg	Lys	Ile	Pro	Gly	Ser	Tyr	Gly	Phe	Pro	Leu	Leu
			20					25				30			
Gly	Pro	Leu	Trp	Asp	Arg	Leu	Asp	Tyr	Asn	Trp	Phe	Gln	Lys	Leu	Pro
		35				40					45				
Asp	Phe	Phe	Ser	Lys	Arg	Val	Glu	Lys	Tyr	Asn	Ser	Thr	Val	Phe	Arg
	50				55					60					
Thr	Asn	Val	Pro	Pro	Cys	Phe	Pro	Phe	Phe	Leu	Gly	Val	Asn	Pro	Asn
65					70					75				80	
Val	Val	Ala	Val	Leu	Asp	Val	Lys	Ser	Phe	Ala	His	Leu	Phe	Asp	Met
			85						90				95		
Glu	Ile	Val	Glu	Lys	Ala	Asn	Val	Leu	Val	Gly	Asp	Phe	Met	Pro	Ser
			100					105				110			
Val	Val	Tyr	Thr	Gly	Asp	Met	Arg	Val	Cys	Ala	Tyr	Leu	Asp	Thr	Ser
		115				120					125				
Glu	Pro	Lys	His	Thr	Gln	Ile	Lys	Asn	Phe	Ser	Leu	Asp	Ile	Leu	Lys
	130					135				140					
Arg	Ser	Ser	Lys	Thr	Trp	Val	Pro	Thr	Leu	Val	Lys	Glu	Leu	Asp	Thr
145					150				155					160	
Leu	Phe	Gly	Thr	Phe	Glu	Ser	Asp	Leu	Ser	Lys	Ser	Lys	Ser	Ala	Ser
			165					170						175	
Leu	Leu	Pro	Ala	Leu	Gln	Lys	Phe	Leu	Phe	Asn	Phe	Phe	Ser	Leu	Thr
			180					185				190			
Phe	Leu	Gly	Ala	Asp	Pro	Ser	Ala	Ser	Pro	Glu	Ile	Ala	Asn	Ser	Gly
	195					200					205				
Phe	Ala	Tyr	Leu	Asp	Ala	Trp	Leu	Ala	Ile	Gln	Leu	Ala	Pro	Thr	Val
	210					215					220				

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<400> 33

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Pro	Thr	Arg	Pro	Ile	Pro	Gly	Ser	Tyr	Gly	Pro	Pro	Leu	Val	Gly	Pro
			20					25					30		
Leu	Lys	Asp	Arg	Leu	Asp	Tyr	Phe	Trp	Phe	Gln	Gly	Pro	Glu	Thr	Phe
		35					40					45			
Phe	Arg	Ser	Arg	Met	Ala	Thr	His	Lys	Ser	Thr	Val	Phe	Arg	Thr	Asn
	50					55					60				
Met	Pro	Pro	Thr	Phe	Pro	Phe	Phe	Val	Gly	Val	Asp	Pro	Arg	Val	Val
65					70					75					80
Thr	Val	Leu	Asp	Cys	Thr	Ser	Phe	Ser	Ala	Leu	Phe	Asp	Leu	Glu	Val
				85					90					95	
Val	Glu	Lys	Lys	Asn	Ile	Leu	Ile	Gly	Asp	Tyr	Met	Pro	Ser	Leu	Ser
			100					105					110		
Phe	Thr	Gly	Asp	Thr	Arg	Val	Val	Val	Tyr	Leu	Asp	Pro	Ser	Glu	Pro
		115					120					125			
Asp	His	Ala	Arg	Val	Lys	Ser	Phe	Cys	Leu	Glu	Leu	Leu	Arg	Arg	Gly
	130					135						140			

Ala Lys Thr Trp Val Ser Ser Phe Leu Ser Asn Leu Asp Val Met Leu
145 150 155 160
Ala Thr Ile Glu Gln Gly Ile Ala Lys Asp Gly Ser Ala Gly Leu Phe
165 170 175
Gly Pro Leu Gln Lys Cys Ile Phe Ala Phe Leu Cys Lys Ser Ile Ile
180 185 190
Gly Ala Asp Pro Ser Val Ser Pro Asp Val Gly Glu Asn Gly Phe Val
195 200 205
Met Leu Asp Lys Trp Leu Ala Leu Gln Leu Leu Pro Thr Val Lys Val
210 215 220
Gly Ala Ile Pro Gln Pro Leu Glu Glu Ile Leu Leu His Ser Phe Pro
225 230 235 240
Leu Pro Phe Phe Leu Val Ser Arg Asp Tyr Arg Lys Leu Tyr Glu Phe
245 250 255
Val Glu Lys Gln Gly Gln Glu Val Val Arg Arg Ala Glu Thr Glu His
260 265 270
Gly Leu Ser Lys His Asp Ala Ile Asn Asn Ile Leu Phe Val Leu Gly
275 280 285
Phe Asn Ala Phe Gly Gly Phe Ser Val Phe Phe Pro Thr Leu Leu Thr
290 295 300
Thr Ile Gly Arg Asp Lys Thr Gly Leu Arg Glu Lys Leu Lys Asp Glu
305 310 315 320
Val Arg Arg Val Met Lys Ser Arg Gly Glu Lys Arg Pro Ser Phe Glu
325 330 335
Thr Val Arg Glu Met Glu Leu Val Arg Ser Thr Val Tyr Glu Val Leu
340 345 350
Arg Leu Asn Pro Pro Val Pro Leu Gln Tyr Gly Arg Ala Arg Thr Asp
355 360 365
Phe Thr Leu Asn Ser His Asp Ala Ala Phe Lys Val Glu Lys Gly Glu
370 375 380
Leu Leu Cys Gly Tyr Gln Pro Leu Val Met Arg Asp Pro Ala Val Phe
385 390 395 400
Asp Asp Pro Glu Thr Phe Ala Pro Glu Arg Phe Met Gly Ser Gly Lys
405 410 415
Glu Leu Leu Lys Tyr Val Phe Trp Ser Asn Gly Pro Glu Thr Gly Thr
420 425 430
Pro Thr Pro Ala Asn Lys Gln Cys Ala Ala Lys Asp Tyr Val Val Glu
435 440 445
Thr Ala Cys Leu Leu Met Ala Glu Ile Phe Tyr Arg Tyr Asp Glu Phe
450 455 460
Val Cys Ala Asp Asp Ala Ile Ser Val Thr Lys Leu Asp Arg Ala Arg
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Glu Trp Glu

<210> 34

<211> 21

<212> DNA

<213> Artificial Sequence

>220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 34

ggttatcagc cgctggtgat g

<210> 35
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 35
 atgaaccgga ggcgtttaat ccg

23

<210> 36
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 36
 acagagcgga cgagttcgta cct

23

<210> 37
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 37
 aggattcgga gaagttcgtg ggc

23

<210> 38
 <211> 488
 <212> PRT
 <213> Psidium guava

<400> 38
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 Tyr Pro Pro Ser Leu Ser Pro Pro Ser Ser Pro Arg Pro Thr Thr Leu
 20 25 30
 Pro Val Arg Thr Ile Pro Gly Ser Tyr Gly Trp Pro Leu Leu Gly Pro
 35 40 45
 Ile Ser Asp Arg Leu Asp Tyr Phe Trp Phe Gln Gly Pro Glu Thr Phe
 50 55 60
 Phe Arg Lys Arg Ile Glu Lys Tyr Lys Ser Thr Val Phe Arg Ala Asn
 65 70 75 80
 Val Pro Pro Cys Phe Pro Phe Phe Ser Asn Val Asn Pro Asn Val Val
 85 90 95
 Val Val Leu Asp Cys Glu Ser Phe Ala His Leu Phe Asp Met Glu Ile
 100 105 110

Val	Glu	Lys	Ser	Asn	Val	Leu	Val	Gly	Asp	Phe	Met	Pro	Ser	Val	Lys
		115					120					125			
Tyr	Thr	Gly	Asn	Ile	Arg	Val	Cys	Ala	Tyr	Leu	Asp	Thr	Ser	Glu	Pro
		130				135					140				
Gln	His	Ala	Gln	Val	Lys	Asn	Phe	Ala	Met	Asp	Ile	Leu	Lys	Arg	Ser
145					150					155					160
Ser	Lys	Val	Trp	Glu	Ser	Glu	Val	Ile	Ser	Asn	Leu	Asp	Thr	Met	Trp
				165					170					175	
Asp	Thr	Ile	Glu	Ser	Ser	Leu	Ala	Lys	Asp	Gly	Asn	Ala	Ser	Val	Ile
			180					185					190		
Phe	Pro	Leu	Gln	Lys	Phe	Leu	Phe	Asn	Phe	Leu	Ser	Lys	Ser	Ile	Ile
		195					200					205			
Gly	Ala	Asp	Pro	Ala	Ala	Ser	Pro	Gln	Val	Ala	Lys	Ser	Gly	Tyr	Ala
		210				215					220				
Met	Leu	Asp	Arg	Trp	Leu	Ala	Leu	Gln	Leu	Leu	Pro	Thr	Ile	Asn	Ile
225					230					235					240
Gly	Val	Leu	Gln	Pro	Leu	Val	Glu	Ile	Phe	Leu	His	Ser	Trp	Ala	Tyr
				245					250					255	
Pro	Phe	Ala	Leu	Val	Ser	Gly	Asp	Tyr	Asn	Lys	Leu	Tyr	Gln	Phe	Ile
			260					265					270		
Glu	Lys	Glu	Gly	Arg	Glu	Ala	Val	Glu	Arg	Ala	Lys	Ala	Glu	Phe	Gly
		275					280					285			
Leu	Thr	His	Gln	Glu	Ala	Ile	His	Asn	Leu	Leu	Phe	Ile	Leu	Gly	Phe
		290				295					300				
Asn	Ala	Phe	Gly	Gly	Phe	Ser	Ile	Phe	Leu	Pro	Thr	Leu	Leu	Ser	Asn
305					310					315					320
Ile	Leu	Ser	Asp	Thr	Thr	Gly	Leu	Gln	Asp	Arg	Leu	Arg	Lys	Glu	Val
				325					330					335	
Arg	Ala	Lys	Gly	Gly	Pro	Ala	Leu	Ser	Phe	Ala	Ser	Val	Lys	Glu	Met
			340					345					350		
Glu	Leu	Val	Lys	Ser	Val	Val	Tyr	Glu	Thr	Leu	Arg	Leu	Asn	Pro	Pro
		355					360					365			
Val	Pro	Phe	Gln	Tyr	Ala	Arg	Ala	Arg	Lys	Asp	Phe	Gln	Leu	Lys	Ser
		370				375				380					
His	Asp	Ser	Val	Phe	Asp	Val	Lys	Lys	Gly	Glu	Leu	Leu	Cys	Gly	Tyr
385					390					395					400
Gln	Lys	Val	Val	Met	Thr	Asp	Pro	Lys	Val	Phe	Asp	Glu	Pro	Glu	Ser
				405					410					415	
Phe	Asn	Ser	Asp	Arg	Phe	Val	Gln	Asn	Ser	Glu	Leu	Leu	Asp	Tyr	Leu
			420					425					430		
Tyr	Trp	Ser	Asn	Gly	Pro	Gln	Thr	Gly	Thr	Pro	Thr	Glu	Ser	Asn	Lys
		435					440					445			
Gln	Cys	Ala	Ala	Lys	Asp	Tyr	Val	Thr	Leu	Thr	Ala	Cys	Leu	Phe	Val
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<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:/Note =

synthetic construct

<400> 39
ccgtcagcac caccaaattcc ttc 23

<210> 40
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 40
gaacagataa tccagcaggg c 21

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 41
ctgaaccgac cgcgactgtg t 21

<210> 42
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 42
tcgcccgtga accgatcagg ta 22

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 43
tccgcgtcgg ctccactgtc 20

<210> 44

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 44
tctcccacga acctatcgcc ca

22

<210> 45
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 45
gccatggcct ccattgtcat tccttc

26

<210> 46
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 46
ggaattctta gtgatggatga tggatgatgga aacttgcttt cttag

45

<210> 47
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 47
gcatatggct actccttctt cctcctc

27

<210> 48
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 48
catcgattta gtgatggtga tggatgatgat tagtcattag ctttaa 46

<210> 49
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 49
atgaattcgg taccgcgggat cctttttttt tttttttt 39

<210> 50
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 50
atgaattcgg taccgcgggat c 21

<210> 51
<211> 1596
<212> DNA
<213> Cucumis melo

<400> 51
atgtcctcca ttgtcattcc ttctcttcaa cctcacttgc gattcccatc ctgcgaagaa 60
acgcctcaaa gatctcggtc tagagtggc ttcgtttcca tacgtccaat ctacgccacc 120
gacggagttt cttcctcgtc ttcttctctc cttcaagtgc cgcagcggat tgtttcgccg 180
ccggaaccca ccaagcttcc tttgaggaag gttcccggtg attatgggcc accgatgttt 240
ggggcggtga aggacagaca tgattatttt tataatcagg ggagggaaga gtatttgaaa 300
tctcgaatgc tccggtatga atccactgtg tatagaacta atatgccgcc ggggtccattt 360
atcacttccg attcccgagt tgttgtttta ctgcacggga agagttttcc tgttcttttc 420
gaccattcta aagttgagaa gaaagatctc tttatcggaa cttacatgcc tgtaacagag 480
ctcaccggcg gttacagggg gctttcttat attgacccat ctgagcccga tcacgctaag 540
cttaaacagt tgattttctt tctcctcaag caccgcgggg ataaaattat gccggaattt 600
cactctactt tttctgagct attcgagact ctggaaaagg atttggctgc tgctggtaga 660
gcagagtaca atgcttccgg tgaacaagcg gcgtttaatt tcttggctcg gtctcttttc 720
ggcgctgac cggtagattc caaattgggt cgcgatgcgc cgaaattgat cgcgaaatgg 780
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gacttctttt acaagtcgtc ggaggcgggtg tttgaggagg cggatagatt gggaatttcg 960
agggaagaag cttgtcaca cttgtatttc acaacttggt ttaattcatt tggagggatg 1020
aagatctttt tccccaatat gataaaatgg atcggccgag ccggagtgaa tctccacacc 1080
cgactagcac gggagattcg tactgccgta aaagccaacg gcgggaaaat cacgatgggg 1140
gctatggaac agatgccgct gatgaaatca gtggtgtacg aagcgtaaag aatcgagccg 1200
ccggttccgg ttcagtacgg tcgggcaaaag aaagaccttg tgggtgaaaag ccacgacgcg 1260
gctttcgaga tcaaaagaag agaagtgatt tgtgggtatc agccattcgc aacaagagat 1320

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<210> 52
<211> 465
<212> PRT
<213> Cucumis melo
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[illegible]

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<210> 53
<211> 468
<212> PRT
<213> Flax
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Leu	Ser	Pro	Ser	Pro	Lys	Ser	Thr	Pro	Leu	Pro	Asn	Thr	Phe	Ser	Asn
			20					25					30		
Leu	Arg	Arg	Val	Ser	Ala	Phe	Arg	Pro	Ile	Lys	Ala	Ser	Leu	Phe	Gly
			35				40					45			
Asp	Ser	Pro	Ile	Lys	Ile	Pro	Gly	Ile	Thr	Ser	Gln	Pro	Pro	Pro	Ser
	50					55					60				
Ser	Asp	Glu	Thr	Thr	Leu	Pro	Ile	Arg	Gln	Ile	Pro	Gly	Asp	Tyr	Gly
65					70					75					80
Leu	Pro	Gly	Ile	Gly	Pro	Ile	Gln	Asp	Arg	Leu	Asp	Tyr	Phe	Tyr	Asn
				85				90						95	
Gln	Gly	Arg	Glu	Glu	Phe	Phe	Lys	Ser	Arg	Leu	Gln	Lys	Tyr	Lys	Ser
			100					105					110		
Thr	Val	Tyr	Arg	Ala	Asn	Met	Pro	Pro	Gly	Pro	Phe	Ile	Ala	Ser	Asn
			115				120					125			
Pro	Arg	Val	Ile	Val	Leu	Leu	Asp	Ala	Lys	Ser	Phe	Pro	Val	Leu	Phe
	130					135					140				
Asp	Met	Ser	Lys	Val	Glu	Lys	Lys	Asp	Leu	Phe	Thr	Gly	Ser	Val	Leu
145					150					155					160
Asp	Glu	Ala	Glu	Gln	Ser	Gly	Ile	Ser	Arg	Asp	Glu	Ala	Cys	His	Asn
				165					170					175	
Ile	Leu	Phe	Ala	Val	Cys	Phe	Asn	Ser	Trp	Gly	Gly	Phe	Lys	Ile	Leu
			180					185					190		
Phe	Pro	Ser	Leu	Met	Lys	Trp	Ile	Gly	Arg	Ala	Gly	Leu	Glu	Leu	His
			195				200					205			
Thr	Lys	Leu	Ala	Gln	Glu	Ile	Arg	Ser	Ala	Ile	Gln	Ser	Thr	Gly	Gly
	210					215					220				
Gly	Lys	Val	Thr	Met	Ala	Ala	Met	Glu	Gln	Met	Pro	Leu	Met	Lys	Ser
225					230					235					240
Val	Val	Tyr	Glu	Thr	Leu	Arg	Ile	Glu	Pro	Pro	Val	Ala	Leu	Gln	Tyr
				245					250					255	
Gly	Lys	Ala	Lys	Lys	Asp	Phe	Ile	Leu	Glu	Ser	His	Glu	Ala	Ala	Tyr
			260					265					270		

Gln Val Lys Glu Gly Glu Met Leu Phe Gly Tyr Gln Pro Phe Ala Thr
 275 280 285
 Lys Asp Pro Lys Ile Phe Asp Arg Pro Glu Glu Phe Val Ala Asp Arg
 290 295 300
 Phe Val Gly Glu Gly Val Lys Leu Met Thr Tyr Met Pro Ser Thr Glu
 305 310 315 320
 Leu Thr Gly Gly Tyr Arg Ile Leu Ser Tyr Leu Asp Pro Ser Glu Pro
 325 330 335
 Asn His Thr Lys Leu Lys Gln Leu Leu Phe Asn Leu Ile Lys Asn Arg
 340 345 350
 Arg Asp Tyr Val Ile Pro Glu Phe Ser Ser Ser Phe Thr Asp Leu Cys
 355 360 365
 Glu Val Val Glu Tyr Asp Leu Ala Thr Lys Gly Lys Ala Ala Phe Asn
 370 375 380
 Asp Pro Ala Glu Gln Ala Ala Phe Asn Phe Leu Ser Arg Ala Phe Phe
 385 390 395 400
 Gly Val Lys Pro Ile Asp Thr Pro Leu Gly Lys Asp Ala Pro Ser Leu
 405 410 415
 Ile Ser Lys Trp Val Leu Phe Asn Leu Ala Pro Ile Leu Ser Val Gly
 420 425 430
 Leu Pro Lys Glu Val Glu Glu Ala Thr Leu His Ser Val Arg Leu Pro
 435 440 445
 Pro Leu Leu Val Gln Asn Asp Tyr His Arg Leu Tyr Glu Phe Phe Thr
 450 455 460
 Ser Ala Ala Gly
 465

<210> 54
 <211> 405
 <212> PRT
 <213> Guayule

<400> 54
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 Ile Pro Phe Phe Gln Pro Ile Lys Asp Arg Leu Glu Tyr Phe Tyr Gly
 20 25 30
 Thr Gly Gly Arg Asp Glu Tyr Phe Arg Ser Arg Met Gln Lys Tyr Gln
 35 40 45
 Ser Thr Val Phe Arg Ala Asn Met Pro Pro Gly Pro Phe Val Ser Ser
 50 55 60
 Asn Pro Lys Val Ile Val Leu Leu Asp Ala Lys Ser Phe Pro Ile Leu
 65 70 75 80
 Phe Asp Val Ser Lys Val Glu Lys Lys Asp Leu Phe Thr Gly Pro Val
 85 90 95
 Met Glu Gln Ala Glu Lys Leu Gly Val Pro Lys Asp Glu Ala Val His
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 Asn Ile Leu Phe Ala Val Cys Phe Asn Thr Phe Gly Gly Val Lys Ile
 115 120 125
 Leu Phe Pro Asn Thr Leu Lys Trp Ile Gly Val Ala Gly Glu Asn Leu
 130 135 140
 His Thr Gln Leu Ala Glu Glu Ile Arg Gly Ala Ile Lys Ser Tyr Gly
 145 150 155 160
 Asp Gly Asn Val Thr Leu Glu Ala Ile Glu Gln Met Pro Leu Thr Lys
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 Ser Val Val Tyr Glu Ser Leu Arg Ile Glu Pro Pro Val Pro Pro Gln
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[illegible]

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Val	Val	Ala	Leu	Leu	Asp	Gly	Lys	Ser	Phe	Pro	Val	Leu	Phe	Asp	Val
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Asp	Lys	Val	Glu	Lys	Lys	Asp	Leu	Phe	Thr	Gly	Glu	Ile	Leu	Val	Glu
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Phe Ala Thr Ser Phe Asn Thr Trp Gly Gly Met Lys Ile Leu Phe Pro
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 Gly Gly Tyr Arg Ile Leu Ser Tyr Leu Asp Pro Ser Glu Pro Lys His
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